BACKGROUND OF THE INVENTION

C1 **1. Field of the Invention**

On page 3, before line 6, insert the following heading:

C2 **2. Description of the Related Art**

On page 4, before line 18, insert the following heading:

C3 **SUMMARY OF THE INVENTION**

On page 5, before line 20, insert the following headings and paragraphs:

BRIEF DESCRIPTION OF THE DRAWINGS

Fig. 1 is a protein sequence of wild-type staphylokinase, SakSTAR (SEQ ID NO: 10). Numbering starts with the NH_2-terminal amino acid of mature full length staphylokinase.

Fig. 2 is a time course of neutralizing activities (left panel) and specific IgG against administered agent (right panel) following intra-arterial infusion of SakSTAR (open

C4 circles, n=9), SakSTAR (K74A) (closed circles, n=11) or SakSTAR (K74A,E75A,R77A) (open squares, n-6) in patients with peripheral arterial occlusion. The data represent median values and interquartile ranges, in μg/ml.

Fig. 3 is a protein sequence of wild-type staphylokinase, SakSTAR with indicated amino acid substitutions.

Squares: single amino acid substitutions; circles: combined (2 to 3) amino acid to Ala substitutions.

Fig. 4 shows temperature stability of SakSTAR, (A); SakSTAR (K74Q, E80A, D82A, K130T, K135R), (B); SakSTAR (E65D, K74R, E80A, D82A, K130T, K135R), (C); and SakSTAR (K35A, E65D, K74Q, E80A, D82A, K130T, K135R), (D).

(○): 4°C; (●): 20°C; (▽): 37°C; (▼): 56°C; (□): 70°C.

Fig. 5 is a time course of neutralizing activities (left panel) and specific IgG against administered agent (right panel) following intra-arterial infusion of SakSTAR (circles, n=15), SakStar (K74Q, E80A, D82A, K130T, K135R) (squares, n=6) or SakSTAR (E65D, K74R, E80A, D82A, K130T, K135R) (triangles, n=6) in patients with peripheral arterial occlusion. The data represent median values and 15-85 percentile ranges, in μg/mL.

C4

DETAILED DESCRIPTION OF THE PREFERRED EMBODIMENTS

On page 9, please delete the first complete paragraph and insert the following replacement paragraph:

The plasmids encloding SakSTAR(K35A,E38A,K74A,E75A), SakSTAR(E38A,E75A,R77A), SakSTAR(E38A,E75A), SakSTAR(K35A,E75A,R77A), SakSTAR(K35A,E75A), SakSTAR(E80A), SakSTAR(D82A), SakSTAR(E75A,D82A), SakSTAR(K74A) and SakSTAR(E75A) were constructed by the spliced overlap extension polymerase chain reaction (SOE-PCR) (24), using Vent DNA polymerase (New England Biolabs, Leusden, The Netherlands), and available or generated *sakSTAR* variants as template. Two fragments were amplified by PCR, the first one starting from the 5' end of the *staphylokinase* gene with primer 5'-CAGGAAACAGAATTCAGGAG-3' (SEQ ID NO: 1) to the region to be mutagenized (forward primer), the second one from the same region (backward primer) to the 3' end of the *staphylokinase* gene with primer 5'-CAAAACAGCCAAGCTTCATTCATTCAGC-3' (SEQ ID NO: 2).

C5

On page 19, please delete the first complete paragraph and insert the following replacement paragraph:

The variants SakSTAR(Y17A,F18A), SakSTAR(F104A), SakSTAR(F111A), SakSTAR(Y9A), SakSTAR(Y91A), SakSTAR(Y92A), SakSTAR(I87A), SakSTAR(I106A) and SakSTAR(I120A) were constructed with the Chameleon Double-Stranded Site-Directed Mutagenesis kit from Stratagene (La Jolla, USA), using the *pMEX.SakSTAR* vector as tmplate, and following instructions of the supplier. The mutagenic oligonucleotides (not shown) were used in combination with the selection-primer LY34 5' CAAAACAGCCGAGCTTCATTCATTCAGC (SEQ ID NO: 3), which destroys the unique *Hind*III site located 3' to the staphylokinase encoding gene in *pMEX.SakSTAR* and allows to C6 counter-select the non-mutant progeny by HindIII digestion. The deletion of the *Hind*III site was in most cases correlated with the presence of the desired mutation introduced by the mutagenic oligonucleotide. The variant SakSTAR(I133A), was constructed by performing a polymerase chain reaction on the *pMEX.SakSTAR* plasmid using the primer 818A located at the 5' end of the *sak*STAR gene (5' CAGGAAACAGAATTCAGGAG) (SEQ ID NO: 1) and the mutagenic primer LY58 (5' TTCAGCATGCTGCAGTTATTTCTTTTCTGCAACAACC TTGG) (SEQ ID NO: 4). The amplified product (30 cycles: 30 sec at 94°C, 30 sec at 50°C, 30 sec at 72°C) was purified, digested with EcoRI and PstI, and ligated into the corresponding sites of *pMEXSakSTAR*.

On page 20, please delete the first complete paragraph and insert the following replacement paragraph:

The plasmids encoding all the other variants listed in Table 3 were contructed by direct PCR C7 or by the spliced overlap extension polymerase chain reaction (SOE-PCR)(24) using *pMEX.SakSTAR* or available plasmids encoding SakSTAR variants as template. Two

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On page 20, please delete the first complete paragraph and insert the following replacement paragraph:

The plasmids encoding all the other variants listed in Table 3 were contructed by direct PCR or by the spliced overlap extension polymerase chain reaction (SOE-PCR)(24) using *pMEX.SakSTAR* or available plasmids encoding SakSTAR variants as template. Two

fragments were amplified by PCR (30 cycles: 1 sec at 94°C, 1 sec at 50°C, 10 sec at 72°C), the first one starting from the 5' end (primer 818A) of the *staphylokinase* gene to the region to be mutagenized (forward primer), the second one from this same region (backward primer) to the 3' end of the gene with primer 818D (5' CAAACAGCCAAGCTTCATTCATTCAGC) (SEQ ID NO: 5). The forward and backward primers shared an overlap of around 24 bp (primers not shown). The two purified fragments were then assembled to gether in a second PCR reaction with the external primers 818A and 818D (30 cycles: 1 sec at 94°C, 1 sec at 50°C, 10 sec at 72°C). The amplified product from this final reaction was purified, digested with EcoRI and HindII and ligated into the corresponding site of *pMEX.SakSTAR*. For each construction, the sequence of the variant was confirmed by sequencing the entire *Sak*STAR coding region.

C7

On page 32, please delete the first complete paragraph and insert the following replacement paragraph:

The variants SakSTAR(K102C) and SakSTAR(K109C), were constructed by the spliced overlap extension polymerase chain reaction (SOE-PCR) (24) using *pMEX.SakSTAR* encoding SakSTAR as template. Two fragments were amplified by PCR (30 cycles: 1 sec at 94°C, 1 sec at 50°C, 10 sec at 72°C), the first one starting from the 5' end (primer 818A) of the *staphylokinase* gene to the region to be mutagenized (forward primer), the second one from this same region (backward primer) to the 3' end of the gene with primer 818D (5' CAAACAGCCAAGCTTCATTCATTCAGC) (SEQ ID NO: 5). The forward and backward primers shared an overlap of around 24 bp (for the contruction of K102C: TAT GAT AAG AAT TGC AAA AAA GAA GAA (backward) (SEQ ID NO: 6) and TTC TTC TTT TTT GCA ATT CTT ATC ATA (forward) (SEQ ID NO: 7) for the construction of K109C: AAA AAG AAG AAA CGT GCT CTT TCC CTA (backward) (SEQ ID NO: 8) and TAG GGA

C8

fragments were amplified by PCR (30 cycles: 1 sec at 94°C, 1 sec at 50°C, 10 sec at 72°C), the first one starting from the 5' end (primer 818A) of the *staphylokinase* gene to the region to be mutagenized (forward primer), the second one from this same region (backward primer) to the 3' end of the gene with primer 818D (5' CAAACAGCCAAGCTTCATTCATTCAGC) (SEQ ID NO: 5). The forward and backward primers shared an overlap of around 24 bp (primers not shown). The two purified fragments were then assembled to gether in a second PCR reaction with the external primers 818A and 818D (30 cycles: 1 sec at 94°C, 1 sec at 50°C, 10 sec at 72°C). The amplified product from this final reaction was purified, digested with EcoRI and HindII and ligated into the corresponding site of *pMEX.SakSTAR*. For each construction, the sequence of the variant was confirmed by sequencing the entire *Sak*STAR coding region.

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